SEQUENCE LISTING

<110> E. I. duPont de Nemours and Company, Inc.
       Suh, Wonchul
       Rouviere, Pierre
       Cheng, Qiong

<120> Increasing Carotenoid Production in Bacteria Via Chromosomal
       Integration

<130> CL2027 US NA

<150> US 60/434618
<151> 2002-12-19

<160> 66

<170> PatentIn version 3.2

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tgcgcggttg aaatggtgca tgctgcctcg ctgattctgg atgatatgcc ctgcatggac   300

gatgcgcaga tgcgtcgggg gcgtcccacc attcacacgc agtacggtga acatgtggcg   360

attctggcgg cggtcgcttt actcagcaaa gcgtttgggg tgattgccga ggctgaaggt   420

ctgacgccga tagccaaaac tcgcgcggtg tcggagctgt ccactgcgat tggcatgcag   480

ggtctggttc agggccagtt taaggacctc tcggaaggcg ataaaccccg cagcgccgat   540

gccatactgc taaccaatca gtttaaaacc agcacgctgt tttgcgcgtc aacgcaaatg   600

gcgtccattg cggccaacgc gtcctgcgaa gcgcgtgaga acctgcatcg tttctcgctc   660

gatctcggcc aggcctttca gttgcttgac gatcttaccg atggcatgac cgataccggc   720

aaagacatca atcaggatgc aggtaaatca acgctggtca atttattagg ctcaggcgcg   780

gtcgaagaac gcctgcgaca gcatttgcgc ctggccagtg aacacctttc cgcggcatgc   840

caaaacggcc attccaccac ccaacttttt attcaggcct ggtttgacaa aaaactcgct   900

gccgtcagtt aa   912

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<213> Pantoea stewartii

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Glu Gln Leu Leu Ala Asp Ile Asp Ser Arg Leu Asp Gln Leu Leu Pro
            20   25   30

Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr
        35   40   45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Leu Thr Ala
    50   55   60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65   70   75   80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
            85   90   95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
            100   105   110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
        115   120   125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
    130   135   140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145   150   155   160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
            165   170   175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
            180   185   190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
        195   200   205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
    210   215   220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225   230   235   240

Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
            245   250   255

Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
            260   265   270

Page 2

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Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln
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Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser
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<213>   Pantoea stewartii


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1               5                   10                  15

gct ctg caa aac ctt gct cag gaa tta gtg gcc cgc ggt cat cgt gtt       96
Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
            20                  25                  30

acg ttt ttt cag caa cat gac tgc aaa gcg ctg gta acg ggc agc gat      144
Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
        35                  40                  45

atc gga ttc cag acc gtc gga ctg caa acg cat cct ccc ggt tcc tta      192
Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
    50                  55                  60

tcg cac ctg ctg cac ctg gcc gcg cac cca ctc gga ccc tcg atg tta      240
Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65              70                  75                  80

cga ctg atc aat gaa atg gca cgt acc agc gat atg ctt tgc cgg gaa      288
Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
                85                  90                  95

ctg ccc gcc gct ttt cat gcg ttg cag ata gag ggc gtg atc gtt gat      336
Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
            100                 105                 110

caa atg gag ccg gca ggt gca gta gtc gca gaa gcg tca ggt ctg ccg      384
Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
            115                 120                 125

ttt gtt tcg gtg gcc tgc gcg ctg ccg ctc aac cgc gaa ccg ggt ttg      432
Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
        130                 135                 140

cct ctg gcg gtg atg cct ttc gag tac ggc acc agc gat gcg gct cgg      480
Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145                 150                 155                 160

gaa cgc tat acc acc agc gaa aaa att tat gac tgg ctg atg cga cgt      528
Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
                165                 170                 175

cac gat cgt gtg atc gcg cat cat gca tgc aga atg ggt tta gcc ccg      576
His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
            180                 185                 190

cgt gaa aaa ctg cat cat tgt ttt tct cca ctg gca caa atc agc cag      624
Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
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Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
        195             200             205

ttg atc ccc gaa ctg gat ttt ccc cgc aaa gcg ctg cca gac tgc ttt    672
Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
        210             215             220

cat gcg gtt gga ccg tta cgg caa ccc cag ggg acg ccg ggg tca tca    720
His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225                 230             235             240

act tct tat ttt ccg tcc ccg gac aaa ccc cgt att ttt gcc tcg ctg    768
Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
                245             250             255

ggc acc ctg cag gga cat cgt tat ggc ctg ttc agg acc atc gcc aaa    816
Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
                260             265             270

gcc tgc gaa gag gtg gat gcg cag tta ctg ttg gca cac tgt ggc ggc    864
Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
            275             280             285

ctc tca gcc acg cag gca ggt gaa ctg gcc cgg ggc ggg gac att cag    912
Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
        290             295             300

gtt gtg gat ttt gcc gat caa tcc gca gca ctt tca cag gca cag ttg    960
Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305             310             315             320

aca atc aca cat ggt ggg atg aat acg gta ctg gac gct att gct tcc   1008
Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
                325             330             335

cgc aca ccg cta ctg gcg ctg ccg ctg gca ttt gat caa cct ggc gtg   1056
Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
                340             345             350

gca tca cga att gtt tat cat ggc atc ggc aag cgt gcg tct cgg ttt   1104
Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
                355             360             365

act acc agc cat gcg ctg gcg cgg cag att cga tcg ctg ctg act aac   1152
Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
        370             375             380

acc gat tac ccg cag cgt atg aca aaa att cag gcc gca ttg cgt ctg   1200
Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385             390             395             400

gca ggc ggc aca cca gcc gcc gcc gat att gtt gaa cag gcg atg cgg   1248
Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
                405             410             415

acc tgt cag cca gta ctc agt ggg cag gat tat gca acc gca cta tga   1296
Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
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<213>    Pantoea stewartii

<400>    4

Met Ser His Phe Ala Val Ile Ala Pro Pro Phe Phe Ser His Val Arg
1               5               10              15
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Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
            20                  25              30

Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
            35                  40              45

Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
    50                  55                  60

Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65                  70                  75                  80

Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
            85                  90                  95

Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
            100                 105                 110

Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
        115                 120                 125

Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
    130                 135                 140

Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145                 150                 155                 160

Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
            165                 170                 175

His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
            180                 185                 190

Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
            195                 200                 205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
    210                 215                 220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225                 230                 235                 240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
            245                 250                 255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
            260                 265                 270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
    275                 280                 285
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Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
    290             295             300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305             310             315             320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
                325             330             335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
            340             345             350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
        355             360             365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
    370             375             380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385             390             395             400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
                405             410             415

Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
            420             425             430


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<213>   Pantoea stewartii


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Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu Ala Asn
1               5                   10                  15

ggc ctt atc gcg ctc cgg ctt cag caa cag cat ccg gat atg cgg atc      96
Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile
            20                  25                  30

ttg ctt att gag gcg ggt cct gag gcg gga ggg aac cat acc tgg tcc     144
Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
        35                  40                  45

ttt cac gaa gag gat tta acg ctg aat cag cat cgc tgg ata gcg ccg     192
Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
    50                  55                  60

ctt gtg gtc cat cac tgg ccc gac tac cag gtt cgt ttc ccc caa cgc     240
Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65                  70                  75                  80

cgt cgc cat gtg aac agt ggc tac tac tgc gtg acc tcc cgg cat ttc     288
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Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
                85                      90                  95

gcc ggg ata ctc cgg caa cag ttt gga caa cat tta tgg ctg cat acc    336
Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
            100                 105                 110

gcg gtt tca gcc gtt cat gct gaa tcg gtc cag tta gcg gat ggc cgg    384
Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
            115                 120                 125

att att cat gcc agt aca gtg atc gac gga cgg ggt tac acg cct gat    432
Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
        130                 135                 140

tct gca cta cgc gta gga ttc cag gca ttt atc ggt cag gag tgg caa    480
Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145                 150                 155                 160

ctg agc gcg ccg cat ggt tta tcg tca ccg att atc atg gat gcg acg    528
Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
                165                 170                 175

gtc gat cag caa aat ggc tac cgc ttt gtt tat acc ctg ccg ctt tcc    576
Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
            180                 185                 190

gca acc gca ctg ctg atc gaa gac aca cac tac att gac aag gct aat    624
Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
            195                 200                 205

ctt cag gcc gaa cgg gcg cgt cag aac att cgc gat tat gct gcg cga    672
Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
        210                 215                 220

cag ggt tgg ccg tta cag acg ttg ctg cgg gaa gaa cag ggt gca ttg    720
Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225                 230                 235                 240

ccc att acg tta acg ggc gat aat cgt cag ttt tgg caa cag caa ccg    768
Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
                245                 250                 255

caa gcc tgt agc gga tta cgc gcc ggg ctg ttt cat ccg aca acc ggc    816
Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
            260                 265                 270

tac tcc cta ccg ctc gcg gtg gcg ctg gcc gat cgt ctc agc gcg ctg    864
Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
            275                 280                 285

gat gtg ttt acc tct tcc tct gtt cac cag acg att gct cac ttt gcc    912
Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
        290                 295                 300

cag caa cgt tgg cag caa cag ggg ttt ttc cgc atg ctg aat cgc atg    960
Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305                 310                 315                 320

ttg ttt tta gcc gga ccg gcc gag tca cgc tgg cgt gtg atg cag cgt    1008
Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
                325                 330                 335

ttc tat ggc tta ccc gag gat ttg att gcc cgc ttt tat gcg gga aaa    1056
Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
            340                 345                 350

ctc acc gtg acc gat cgg cta cgc att ctg agc ggc aag ccg ccc gtt    1104
Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
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            355                    360                    365
ccc gtt ttc gcg gca ttg cag gca att atg acg act cat cgt tga          1149
Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
    370                    375                    380
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<213> Pantoea stewartii

<400> 6

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Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile
            20                  25                  30

Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
            35                  40                  45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
    50                  55                  60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65                  70                  75                  80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
                85                  90                  95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
            100                 105                 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
            115                 120                 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
    130                 135                 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145                 150                 155                 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
                165                 170                 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
            180                 185                 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
            195                 200                 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
    210                 215                 220
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Page 8

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Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225             230             235             240

Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
                245             250             255

Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
            260             265             270

Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
        275             280             285

Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
    290             295             300

Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305             310             315             320

Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
                325             330             335

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
            340             345             350

Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
            355             360             365

Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
    370             375             380
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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
1               5               10              15

gca att cgt tta cag gcc gca ggt att cct gtt ttg ctg ctt gag cag       96
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
            20              25              30

cgc gac aag ccg ggt ggc cgg gct tat gtt tat cag gag cag ggc ttt      144
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
        35              40              45

act ttt gat gca ggc cct acc gtt atc acc gat ccc agc gcg att gaa      192
Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
    50              55              60

gaa ctg ttt gct ctg gcc ggt aaa cag ctt aag gat tac gtc gag ctg      240
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Page 9

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Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
65              70              75              80

ttg ccg gtc acg ccg ttt tat cgc ctg tgc tgg gag tcc ggc aag gtc    288
Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
                85              90              95

ttc aat tac gat aac gac cag gcc cag tta gaa gcg cag ata cag cag    336
Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
            100             105             110

ttt aat ccg cgc gat gtt gcg ggt tat cga gcg ttc ctt gac tat tcg    384
Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
            115             120             125

cgt gcc gta ttc aat gag ggc tat ctg aag ctc ggc act gtg cct ttt    432
Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
        130             135             140

tta tcg ttc aaa gac atg ctt cgg gcc gcg ccc cag ttg gca aag ctg    480
Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145             150             155             160

cag gca tgg cgc agc gtt tac agt aaa gtt gcc ggc tac att gag gat    528
Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
                165             170             175

gag cat ctt cgg cag gcg ttt tct ttt cac tcg ctc tta gtg ggg ggg    576
Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
            180             185             190

aat ccg ttt gca acc tcg tcc att tat acg ctg att cac gcg tta gaa    624
Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
            195             200             205

cgg gaa tgg ggc gtc tgg ttt cca cgc ggt gga acc ggt gcg ctg gtc    672
Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
    210             215             220

aat ggc atg atc aag ctg ttt cag gat ctg ggc ggc gaa gtc gtg ctt    720
Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225             230             235             240

aac gcc cgg gtc agt cat atg gaa acc gtt ggg gac aag att cag gcc    768
Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
                245             250             255

gtg cag ttg gaa gac ggc aga cgg ttt gaa acc tgc gcg gtg gcg tcg    816
Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
                260             265             270

aac gct gat gtt gta cat acc tat cgc gat ctg ctg tct cag cat ccc    864
Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
            275             280             285

gca gcc gct aag cag gcg aaa aaa ctg caa tcc aag cgt atg agt aac    912
Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
    290             295             300

tca ctg ttt gta ctc tat ttt ggt ctc aac cat cat cac gat caa ctc    960
Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305             310             315             320

gcc cat cat acc gtc tgt ttt ggg cca cgc tac cgt gaa ctg att cac    1008
Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
            325             330             335

gaa att ttt aac cat gat ggt ctg gct gag gat ttt tcg ctt tat tta    1056
Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
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cac gca cct tgt gtc acg gat ccg tca ctg gca ccg gaa ggg tgc ggc      1104
His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
        355             360             365

agc tat tat gtg ctg gcg cct gtt cca cac tta ggc acg gcg aac ctc      1152
Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
    370             375             380

gac tgg gcg gta gaa gga ccc cga ctg cgc gat cgt att ttt gac tac      1200
Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
385             390             395             400

ctt gag caa cat tac atg cct ggc ttg cga agc cag ttg gtg acg cac      1248
Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
            405             410             415

cgt atg ttt acg ccg ttc gat ttc cgc gac gag ctc aat gcc tgg caa      1296
Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
            420             425             430

ggt tcg gcc ttc tcg gtt gaa cct att ctg acc cag agc gcc tgg ttc      1344
Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
            435             440             445

cga cca cat aac cgc gat aag cac att gat aat ctt tat ctg gtt ggc      1392
Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
    450             455             460

gca ggc acc cat cct ggc gcg ggc att ccc ggc gta atc ggc tcg gcg      1440
Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465             470             475             480

aag gcg acg gca ggc tta atg ctg gag gac ctg att tga                  1479
Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
            485             490
```

<210> 8
<211> 492
<212> PRT
<213> Pantoea stewartii

<400> 8

```
Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
1               5               10              15


Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
            20              25              30


Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
        35              40              45


Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
    50              55              60


Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
65              70              75              80


Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
            85              90              95
```

```
Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
            100                 105                 110

Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
            115                 120                 125

Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
    130                 135                 140

Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145                 150                 155                 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
                165                 170                 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
                180                 185                 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
                195                 200                 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
    210                 215                 220

Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225                 230                 235                 240

Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
                245                 250                 255

Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
            260                 265                 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
            275                 280                 285

Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
    290                 295                 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305                 310                 315                 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
                325                 330                 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
            340                 345                 350

His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
        355                 360                 365
```

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```
Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
    370             375                 380

Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
385             390                 395                 400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
                405                 410                 415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
            420                 425                 430

Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
            435                 440                 445

Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
    450                 455                 460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465                 470                 475                 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
                485                 490
```

<210> 9
<211> 891
<212> DNA
<213> Pantoea stewartii

<220>
<221> CDS
<222> (1)..(891)

<400> 9
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atg gcg gtt ggc tcg aaa agc ttt gcg act gca tcg acg ctt ttc gac       48
Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1               5                   10                  15

gcc aaa acc cgt cgc agc gtg ctg atg ctt tac gca tgg tgc cgc cac       96
Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
                20                  25                  30

tgc gac gac gtc att gac gat caa aca ctg ggc ttt cat gcc gac cag      144
Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
            35                  40                  45

ccc tct tcg cag atg cct gag cag cgc ctg cag cag ctt gaa atg aaa      192
Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
    50                  55                  60

acg cgt cag gcc tac gcc ggt tcg caa atg cac gag ccc gct ttt gcc      240
Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65                  70                  75                  80

gcg ttt cag gag gtc gcg atg gcg cat gat atc gct ccc gcc tac gcg      288
Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
                85                  90                  95

ttc gac cat ctg gaa ggt ttt gcc atg gat gtg cgc gaa acg cgc tac      336
Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
```
Page 13

```
                  100                    105                         110

ctg aca ctg gac gat acg ctg cgt tat tgc tat cac gtc gcc ggt gtt       384
Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
        115             120                 125

gtg ggc ctg atg atg gcg caa att atg ggc gtt cgc gat aac gcc acg       432
Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
        130             135                 140

ctc gat cgc gcc tgc gat ctc ggg ctg gct ttc cag ttg acc aac att       480
Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145             150             155                 160

gcg cgt gat att gtc gac gat gct cag gtg ggc cgc tgt tat ctg cct       528
Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
                165             170                 175

gaa agc tgg ctg gaa gag gaa gga ctg acg aaa gcg aat tat gct gcg       576
Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
        180             185                 190

cca gaa aac cgg cag gcc tta agc cgt atc gcc ggg cga ctg gta cgg       624
Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
        195             200                 205

gaa gcg gaa ccc tat tac gta tca tca atg gcc ggt ctg gca caa tta       672
Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
        210             215                 220

ccc tta cgc tcg gcc tgg gcc atc gcg aca gcg aag cag gtg tac cgt       720
Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225             230             235                 240

aaa att ggc gtg aaa gtt gaa cag gcc ggt aag cag gcc tgg gat cat       768
Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
                245             250                 255

cgc cag tcc acg tcc acc gcc gaa aaa tta acg ctt ttg ctg acg gca       816
Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
        260             265                 270

tcc ggt cag gca gtt act tcc cgg atg aag acg tat cca ccc cgt cct       864
Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
        275             280                 285

gct cat ctc tgg cag cgc ccg atc tag                                   891
Ala His Leu Trp Gln Arg Pro Ile
    290             295


<210>  10
<211>  296
<212>  PRT
<213>  Pantoea stewartii

<400>  10

Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1               5               10              15


Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
            20              25              30


Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
        35              40              45
```

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```
Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
    50              55              60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65              70              75              80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
                85              90              95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
            100             105             110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
        115             120             125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
    130             135             140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145             150             155             160

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
            165             170             175

Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
        180             185             190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
        195             200             205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
    210             215             220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225             230             235             240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
            245             250             255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
            260             265             270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
        275             280             285

Ala His Leu Trp Gln Arg Pro Ile
    290             295

<210>    11
<211>    528
<212>    DNA
<213>    Pantoea stewartii
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<220>
<221> CDS
<222> (1)..(528)

<400> 11

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atg ttg tgg att tgg aat gcc ctg atc gtg ttt gtc acc gtg gtc ggc     48
Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1               5                   10                  15

atg gaa gtg gtt gct gca ctg gca cat aaa tac atc atg cac ggc tgg     96
Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
                20                  25                  30

ggt tgg ggc tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gca ttt    144
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
            35                  40                  45

gaa gtt aac gat ctc tat gcc gtg gta ttc gcc att gtg tcg att gcc    192
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
        50                  55                  60

ctg att tac ttc ggc agt aca gga atc tgg ccg ctc cag tgg att ggt    240
Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65                  70                  75                  80

gca ggc atg acc gct tat ggt tta ctg tat ttt atg gtc cac gac gga    288
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
                85                  90                  95

ctg gta cac cag cgc tgg ccg ttc cgc tac ata ccg cgc aaa ggc tac    336
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
                100                 105                 110

ctg aaa cgg tta tac atg gcc cac cgt atg cat cat gct gta agg gga    384
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
            115                 120                 125

aaa gag ggc tgc gtg tcc ttt ggt ttt ctg tac gcg cca ccg tta tct    432
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
        130                 135                 140

aaa ctt cag gcg acg ctg aga gaa agg cat gcg gct aga tcg ggc gct    480
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145                 150                 155                 160

gcc aga gat gag cag gac ggg gtg gat acg tct tca tcc ggg aag taa    528
Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
                165                 170                 175
```

<210> 12
<211> 175
<212> PRT
<213> Pantoea stewartii

<400> 12

```
Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1               5                   10                  15


Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
                20                  25                  30


Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
            35                  40                  45
```

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```
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
    50                  55              60
```

```
Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65                  70              75                  80
```

```
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
            85              90                  95
```

```
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
            100             105             110
```

```
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
        115             120             125
```

```
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
    130             135             140
```

```
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145             150             155             160
```

```
Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
            165             170             175
```

```
<210>   13
<211>   1860
<212>   DNA
<213>   Methylomonas 16a


<220>
<221>   CDS
<222>   (1)..(1860)

<400>   13
atg gct ctt tcc aaa gac ttc cct cta ctc aat tcc atc cac acc cca        48
Met Ala Leu Ser Lys Asp Phe Pro Leu Leu Asn Ser Ile His Thr Pro
1               5                   10                  15

gcg gac ata cgc gcg ctg tcc aag gac cag ctc cag caa ctg gct gac        96
Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp
                20                  25                  30

gag gtg cgc ggc tat ctg acc cac acg gtc agc att tcc ggc ggc cat       144
Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
            35                  40                  45

ttt gcg gcc ggc ctc ggc acc gtg gaa ctg acc gtg gcc ttg cat tat       192
Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
        50                  55                  60

gtg ttc aat acc ccc gtc gat cag ttg gtc tgg gac gtg ggc cat cag       240
Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
65                  70                  75                  80

gcc tat ccg cac aag att ctg acc ggt cgc aag gag cgc atg ccg acc       288
Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
                85                  90                  95
```

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```
att cgc acc ctg ggc ggg gtg tca gcc ttt ccg gcg cgg gac gag agc        336
Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
        100                 105                 110

gaa tac gat gcc ttc ggc gtc ggc cat tcc agc acc tcg atc agc gcg        384
Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
        115                 120                 125

gca ctg ggc atg gcc att gcg tcg cag ctg cgc ggc gaa gac aag aag        432
Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
        130                 135                 140

atg gta gcc atc atc ggc gac ggt tcc atc acc ggc ggc atg gcc tat        480
Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr
145                 150                 155                 160

gag gcg atg aat cat gcc ggc gat gtg aat gcc aac ctg ctg gtg atc        528
Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
                165                 170                 175

ttg aac gac aac gat atg tcg atc tcg ccg ccg gtc ggg gcg atg aac        576
Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
                180                 185                 190

aat tat ctg acc aag gtg ttg tcg agc aag ttt tat tcg tcg gtg cgg        624
Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
        195                 200                 205

gaa gag agc aag aaa gct ctg gcc aag atg ccg tcg gtg tgg gaa ctg        672
Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
        210                 215                 220

gcg cgc aag acc gag gaa cac gtg aag ggc atg atc gtg ccc ggt acc        720
Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
225                 230                 235                 240

ttg ttc gag gaa ttg ggc ttc aat tat ttc ggc ccg atc gac ggc cat        768
Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
                245                 250                 255

gat gtc gag atg ctg gtg tcg acc ctg gaa aat ctg aag gat ttg acc        816
Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
                260                 265                 270

ggg ccg gta ttc ctg cat gtg gtg acc aag aag ggc aaa ggc tat gcg        864
Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
        275                 280                 285

cca gcc gag aaa gac ccg ttg gcc tac cat ggc gtg ccg gct ttc gat        912
Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
        290                 295                 300

ccg acc aag gat ttc ctg ccc aag gcg gcg ccg tcg ccg cat ccg acc        960
Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
305                 310                 315                 320

tat acc gag gtg ttc ggc cgc tgg ctg tgc gac atg gcg gct caa gac       1008
Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
                325                 330                 335

gag cgc ttg ctg ggc atc acg ccg gcg atg cgc gaa ggc tct ggt ttg       1056
Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
        340                 345                 350

gtg gaa ttc tca cag aaa ttt ccg aat cgc tat ttc gat gtc gcc atc       1104
Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
        355                 360                 365

gcc gag cag cat gcg gtg acc ttg gcc gcc ggc cag gcc tgc cag ggc       1152
                        Page 18
```

```
Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
    370                 375             380

gcc aag ccg gtg gtg gcg att tat tcc acc ttc ctg caa cgc ggt tac    1200
Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
385                 390             395             400

gat cag ttg atc cac gac gtg gcc ttg cag aac tta gat atg ctc ttt    1248
Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
                405             410             415

gca ctg gat cgt gcc ggc ttg gtc ggc ccg gat gga ccg acc cat gct    1296
Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
            420             425             430

ggc gcc ttt gat tac agc tac atg cgc tgt att ccg aac atg ctg atc    1344
Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
            435             440             445

atg gct cca gcc gac gag aac gag tgc agg cag atg ctg acc acc ggc    1392
Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
    450             455             460

ttc caa cac cat ggc ccg gct tcg gtg cgc tat ccg cgc ggc aaa ggg    1440
Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
465             470             475             480

ccc ggg gcg gca atc gat ccg acc ctg acc gcg ctg gag atc ggc aag    1488
Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
                485             490             495

gcc gaa gtc aga cac cac ggc agc cgc atc gcc att ctg gcc tgg ggc    1536
Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
                500             505             510

agc atg gtc acg cct gcc gtc gaa gcc ggc aag cag ctg ggc gcg acg    1584
Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
            515             520             525

gtg gtg aac atg cgt ttc gtc aag ccg ttc gat caa gcc ttg gtg ctg    1632
Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
    530             535             540

gaa ttg gcc agg acg cac gat gtg ttc gtc acc gtc gag gaa aac gtc    1680
Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545             550             555             560

atc gcc ggc ggc gct ggc agt gcg atc aac acc ttc ctg cag gcg cag    1728
Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
                565             570             575

aag gtg ctg atg ccg gtc tgc aac atc ggc ctg ccc gac cgc ttc gtc    1776
Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
            580             585             590

gag caa ggt agt cgc gag gaa ttg ctc agc ctg gtc ggc ctc gac agc    1824
Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
            595             600             605

aag ggc atc ttc gcc acc atc gaa cag ttt tgc gct                    1860
Lys Gly Ile Phe Ala Thr Ile Glu Gln Phe Cys Ala
610             615             620


<210>   14
<211>   620
<212>   PRT
<213>   Methylomonas 16a
```

<400> 14

Met Ala Leu Ser Lys Asp Phe Pro Leu Leu Asn Ser Ile His Thr Pro
1   5   10   15

Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp
            20   25   30

Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
        35   40   45

Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
    50   55   60

Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
65   70   75   80

Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
            85   90   95

Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
            100   105   110

Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
        115   120   125

Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
    130   135   140

Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr
145   150   155   160

Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
            165   170   175

Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
            180   185   190

Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
        195   200   205

Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
    210   215   220

Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
225   230   235   240

Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
            245   250   255

Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
            260   265   270

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Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
        275   280   285

Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
    290   295   300

Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
305   310   315   320

Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
            325   330   335

Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
        340   345   350

Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
        355   360   365

Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
    370   375   380

Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
385   390   395   400

Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
            405   410   415

Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
            420   425   430

Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
        435   440   445

Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
    450   455   460

Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
465   470   475   480

Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
            485   490   495

Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
        500   505   510

Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
        515   520   525

Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
    530   535   540

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Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545   550   555   560

Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
                565   570   575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
            580   585   590

Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
        595   600   605

Lys Gly Ile Phe Ala Thr Ile Glu Gln Phe Cys Ala
    610   615   620

<210>   15
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<212>   DNA
<213>   Methylomonas 16a

<220>
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<222>   (22)..(975)

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cccagtaaaa cactcaagaa t atg caa atc gta ctc gca aac ccc cgt gga   51
                        Met Gln Ile Val Leu Ala Asn Pro Arg Gly
                        1   5   10

ttc tgt gcc ggc gtg gac cgg gcc att gaa att gtc gat caa gcc atc   99
Phe Cys Ala Gly Val Asp Arg Ala Ile Glu Ile Val Asp Gln Ala Ile
            15   20   25

gaa gcc ttt ggt gcg ccg att tat gtg cgg cac gag gtg gtg cat aac   147
Glu Ala Phe Gly Ala Pro Ile Tyr Val Arg His Glu Val Val His Asn
            30   35   40

cgc acc gtg gtc gat gga ctg aaa caa aaa ggt gcg gtg ttc atc gag   195
Arg Thr Val Val Asp Gly Leu Lys Gln Lys Gly Ala Val Phe Ile Glu
            45   50   ·55

gaa cta agc gat gtg ccg gtg ggt tcc tac ttg att ttc agc gcg cac   243
Glu Leu Ser Asp Val Pro Val Gly Ser Tyr Leu Ile Phe Ser Ala His
    60   65   70

ggc gta tcc aag gag gtg caa cag gaa gcc gag gag cgc cag ttg acg   291
Gly Val Ser Lys Glu Val Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr
75   80   85   90

gta ttc gat gcg act tgt ccg ctg gtg acc aaa gtg cac atg cag gtt   339
Val Phe Asp Ala Thr Cys Pro Leu Val Thr Lys Val His Met Gln Val
            95   100   105

gcc aag cat gcc aaa cag ggc cga gaa gtg att ttg atc ggc cac gcc   387
Ala Lys His Ala Lys Gln Gly Arg Glu Val Ile Leu Ile Gly His Ala
            110   115   120

ggt cat ccg gaa gtg gaa ggc acg atg ggc cag tat gaa aaa tgc acc   435
Gly His Pro Glu Val Glu Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr
            125   130   135

gaa ggc ggc ggc att tat ctg gtc gaa act ccg gaa gac gta cgc aat   483
Glu Gly Gly Gly Ile Tyr Leu Val Glu Thr Pro Glu Asp Val Arg Asn
                        Page 22

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ttg aaa gtc aac aat ccc aat gat ctg gcc tat gtg acg cag acg acc    531
Leu Lys Val Asn Asn Pro Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr
155             160             165                     170

ttg tcg atg acc gac acc aag gtc atg gtg gat gcg tta cgc gaa caa    579
Leu Ser Met Thr Asp Thr Lys Val Met Val Asp Ala Leu Arg Glu Gln
                175             180             185

ttt ccg tcc att aag gag caa aaa aag gac gat att tgt tac gcg acg    627
Phe Pro Ser Ile Lys Glu Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr
            190             195             200

caa aac cgt cag gat gcg gtg cat gat ctg gcc aag att tcc gac ctg    675
Gln Asn Arg Gln Asp Ala Val His Asp Leu Ala Lys Ile Ser Asp Leu
            205             210             215

att ctg gtt gtc ggc tct ccc aat agt tcg aat tcc aac cgt ttg cgt    723
Ile Leu Val Val Gly Ser Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg
            220             225             230

gaa atc gcc gtg caa ctc ggt aaa ccc gct tat ttg atc gat act tac    771
Glu Ile Ala Val Gln Leu Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr
235             240             245                     250

cag gat ttg aag caa gat tgg ctg gag gga att gaa gta gtc ggg gtt    819
Gln Asp Leu Lys Gln Asp Trp Leu Glu Gly Ile Glu Val Val Gly Val
            255             260             265

acc gcg ggc gct tcg gcg ccg gaa gtg ttg gtg cag gaa gtg atc gat    867
Thr Ala Gly Ala Ser Ala Pro Glu Val Leu Val Gln Glu Val Ile Asp
            270             275             280

caa ctg aag gca tgg ggc ggc gaa acc act tcg gtc aga gaa aac agc    915
Gln Leu Lys Ala Trp Gly Gly Glu Thr Thr Ser Val Arg Glu Asn Ser
            285             290             295

ggc atc gag gaa aag gta gtc ttt tcg att ccc aag gag ttg aaa aaa    963
Gly Ile Glu Glu Lys Val Val Phe Ser Ile Pro Lys Glu Leu Lys Lys
300             305             310

cat atg caa gcg tgatcaa                                            982
His Met Gln Ala
315


<210>   16
<211>   318
<212>   PRT
<213>   Methylomonas 16a

<400>   16

Met Gln Ile Val Leu Ala Asn Pro Arg Gly Phe Cys Ala Gly Val Asp
1               5               10              15


Arg Ala Ile Glu Ile Val Asp Gln Ala Ile Glu Ala Phe Gly Ala Pro
                20              25              30


Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly
                35              40              45


Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro
        50              55              60
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Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val
65   70   75   80

Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys
              85   90   95

Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln
              100   105   110

Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
          115   120   125

Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Gly Ile Tyr
    130   135   140

Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro
145   150   155   160

Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr
              165   170   175

Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu
          180   185   190

Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala
    195   200   205

Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser
    210   215   220

Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu
225   230   235   240

Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp
              245   250   255

Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala
          260   265   270

Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly
          275   280   285

Gly Glu Thr Thr Ser Val Arg Glu Asn Ser Gly Ile Glu Glu Lys Val
    290   295   300

Val Phe Ser Ile Pro Lys Glu Leu Lys Lys His Met Gln Ala
305   310   315

<210>   17
<211>   1254
<212>   DNA
<213>   Methylomonas 16a

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<220>
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<222> (73)..(1254)

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gagcgtattc ga atg aaa ggt att tgc ata ttg ggc gct acc ggt tcg atc   111
              Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile
              1   5   10

ggt gtc agc acg ctg gat gtc gtt gcc agg cat ccg gat aaa tat caa   159
Gly Val Ser Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln
    15   20   25

gtc gtt gcg ctg acc gcc aac ggc aat atc gac gca ttg tat gaa caa   207
Val Val Ala Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln
30   35   40   45

tgc ctg gcc cac cat ccg gag tat gcg gtg gtg gtc atg gaa agc aag   255
Cys Leu Ala His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys
            50   55   60

gta gca gag ttc aaa cag cgc att gcc gct tcg ccg gta gcg gat atc   303
Val Ala Glu Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile
            65   70   75

aag gtc ttg tcg ggt agc gag gcc ttg caa cag gtg gcc acg ctg gaa   351
Lys Val Leu Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu
        80   85   90

aac gtc gat acg gtg atg gcg gct atc gtc ggc gcg gcc gga ttg ttg   399
Asn Val Asp Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu
        95   100   105

ccg acc ttg gcc gcg gcc aag gcc ggc aaa acc gtg ctg ttg gcc aac   447
Pro Thr Leu Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn
110   115   120   125

aag gaa gcc ttg gtg atg tcg gga caa atc ttc atg cag gcc gtc agc   495
Lys Glu Ala Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser
            130   135   140

gat tcc ggc gct gtg ttg ctg ccg ata gac agc gag cac aac gcc atc   543
Asp Ser Gly Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile
            145   150   155

ttt cag tgc atg ccg gcg ggt tat acg cca ggc cat aca gcc aaa cag   591
Phe Gln Cys Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln
            160   165   170

gcg cgc cgc att tta ttg acc gct tcc ggt ggc cca ttt cga cgg acg   639
Ala Arg Arg Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr
    175   180   185

ccg ata gaa acg ttg tcc agc gtc acg ccg gat cag gcc gtt gcc cat   687
Pro Ile Glu Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His
190   195   200   205

cct aaa tgg gac atg ggg cgc aag att tcg gtc gat tcc gcc acc atg   735
Pro Lys Trp Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met
            210   215   220

atg aac aaa ggt ctc gaa ctg atc gaa gcc tgc ttg ttg ttc aac atg   783
Met Asn Lys Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met
            225   230   235

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gag ccc gac cag att gaa gtc gtc att cat ccg cag agc atc att cat      831
Glu Pro Asp Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His
        240             245                 250

tcg atg gtg gac tat gtc gat ggt tcg gtt ttg gcg cag atg ggt aat      879
Ser Met Val Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn
        255             260                 265

ccc gac atg cgc acg ccg ata gcg cac gcg atg gcc tgg ccg gaa cgc      927
Pro Asp Met Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg
270             275                 280                 285

ttt gac tct ggt gtg gcg ccg ctg gat att ttc gaa gta ggg cac atg      975
Phe Asp Ser Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met
            290                 295                 300

gat ttc gaa aaa ccc gac ttg aaa cgg ttt cct tgt ctg aga ttg gct     1023
Asp Phe Glu Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala
        305             310                 315

tat gaa gcc atc aag tct ggt gga att atg cca acg gta ttg aac gca     1071
Tyr Glu Ala Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala
        320             325                 330

gcc aat gaa att gct gtc gaa gcg ttt tta aat gaa gaa gtc aaa ttc     1119
Ala Asn Glu Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe
        335             340                 345

act gac atc gcg gtc atc atc gag cgc agc atg gcc cag ttt aaa ccg     1167
Thr Asp Ile Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro
350             355                 360                 365

gac gat gcc ggc agc ctc gaa ttg gtt ttg cag gcc gat caa gat gcg     1215
Asp Asp Ala Gly Ser Leu Glu Leu Val Leu Gln Ala Asp Gln Asp Ala
            370                 375                 380

cgc gag gtg gct aga gac atc atc aag acc ttg gta gct                 1254
Arg Glu Val Ala Arg Asp Ile Ile Lys Thr Leu Val Ala
            385             390


<210>   18
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<212>   PRT
<213>   Methylomonas 16a

<400>   18

Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile Gly Val Ser
1               5                   10                  15


Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln Val Val Ala
            20                  25                  30


Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
        35                  40                  45


His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu
        50                  55                  60


Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
65                  70                  75                  80


Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
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Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
            100   105   110

Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
            115   120   125

Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
    130   135   140

Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
145   150   155   160

Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
                165   170   175

Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
            180   185   190

Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
        195   200   205

Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
    210   215   220

Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
225   230   235   240

Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
            245   250   255

Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
            260   265   270

Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
        275   280   285

Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu
    290   295   300

Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala
305   310   315   320

Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu
            325   330   335

Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe Thr Asp Ile
            340   345   350

Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala
    355   360   365

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Gly Ser Leu Glu Leu Val Leu Gln Ala Asp Gln Asp Ala Arg Glu Val
    370             375             380

Ala Arg Asp Ile Ile Lys Thr Leu Val Ala
385             390


<210>  19
<211>  25
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Primer #1 for amplification of crt gene cluster

<400>  19
atgacggtct gcgcaaaaaa acacg                                          25


<210>  20
<211>  28
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Primer #2 for amplification of crt gene cluster

<400>  20
gagaaattat gttgtggatt tggaatgc                                       28


<210>  21
<211>  61
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Primer 5'kan(dxs)

<400>  21
tggaagcgct agcggactac atcatccagc gtaataaata acgtcttgag cgattgtgta    60

g                                                                    61


<210>  22
<211>  65
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Primer 5'kan(idi)

<400>  22
tctgatgcgc aagctgaaga aaaatgagca tggagaataa tatgacgtct tgagcgattg    60

tgtag                                                                65


<210>  23
<211>  65
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Primer 5'kan(ygbBP)
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<400> 23
gacgcgtcga agcgcgcaca gtctgcgggg caaaacaatc gataacgtct tgagcgattg   60

tgtag   65

<210> 24
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(ispAdxs)

<400> 24
accatgacgg ggcgaaaaat attgagagtc agacattcat gtgtaggctg gagctgcttc   60

<210> 25
<211> 64
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'kan

<400> 25
gaagacgaaa gggcctcgtg atacgcctat ttttataggt tatatgaata tcctccttag   60

ttcc   64

<210> 26
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-T5

<400> 26
ctaaggagga tattcatata acctataaaa ataggcgtat cacgaggccc   50

<210> 27
<211> 70
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(dxs)

<400> 27
ggagtcgacc agtgccaggg tcgggtattt ggcaatatca aaactcatag ttaatttctc   60

ctctttaatg   70

<210> 28
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(idi)

<400> 28
tgggaactcc ctgtgcattc aataaaatga cgtgttccgt ttgcatagtt aatttctcct   60

ctttaatg   68

<210>   29
<211>   68
<212>   DNA
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<220>
<223>   Primer 3'-T5(ygbBP)

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cggccgccgg aaccacggcg caaacatcca aatgagtggt tgccatagtt aatttctcct   60

ctttaatg   68

<210>   30
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<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer 3'-T5(ispAdxs)

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cctgcttaac gcaggcttcg agttgctgcg gaaagtccat agttaatttc tcctctttaa   60

tg   62

<210>   31
<211>   65
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer 5'-kanT5(ispB)

<400>   31
accataaacc ctaagttgcc tttgttcaca gtaaggtaat cggggcgtct tgagcgattg   60

tgtag   65

<210>   32
<211>   67
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer 3'-kanT5(ispB)

<400>   32
cgccatatct tgcgcggtta actcattgat tttttctaaa ttcatagtta atttctcctc   60

tttaatg   67

<210>   33
<211>   156
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Phage T5 promoter sequence

<400>   33

ctataaaaat aggcgtatca cgaggccctt tcgtcttcac ctcgagaaat cataaaaaat   60

ttatttgctt tgtgagcgga taacaattat aatagattca attgtgagcg gataacaatt   120

tcacacagaa ttcattaaag aggagaaatt aactca   156

<210>   34
<211>   65
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer 5'-kanT5(dxs16a)

<400>   34
cactaacgcc cgcacattgc tgcgggcttt ttgattcatt tcgcacgtct tgagcgattg   60

tgtag   65

<210>   35
<211>   65
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer 5'-kanT5(dxr16a)

<400>   35
taaagggcta agagtagtgt gctcttagcc cttaattacg tttcccgtct tgagcgattg   60

tgtag   65

<210>   36
<211>   65
<212>   DNA
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<220>
<223>   Primer 5'-kanT5(lytB16a)

<400>   36
ctacaactgg cgagatgcat agcgagtata atttgtattt tgcgtcgtct tgagcgattg   60

tgtag   65

<210>   37
<211>   51
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer 3'-kanT5(dxs16a)

<400>   37
agtagaggga agtctttgga aagagccata gttaatttct cctctttaat g   51

<210>   38
<211>   51
<212>   DNA
<213>   Artificial sequence

<220>
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<400> 38
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<210> 39
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-kanT5(lytB16a)

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ccacgggggt ttgcgagtac gatttgcata gttaatttct cctctttaat g   51

<210> 40
<211> 55
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<220>
<223> Primer 5'-(dxs16a)

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<210> 41
<211> 55
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-(dxr16a)

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<210> 42
<211> 55
<212> DNA
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<220>
<223> Primer 5'-(lytB16a)

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acagaattca ttaaagagga gaaattaact atgcaaatcg tactcgcaaa ccccc   55

<210> 43
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<220>
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gttcgatg   68

<210> 44
<211> 67
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<220>
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cttgatg   67

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<211> 68
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<220>
<223> Primer 3'-(lytB16a)

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atatgttt   68

<210> 46
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<212> DNA
<213> Artificial sequence

<220>
<223> Primer T-kan

<400> 46
accggatatc accacttatc tgctc   25

<210> 47
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<220>
<223> Primer B-ispA

<400> 47
cctaataatg cgccatactg catgg   25

<210> 48
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<212> DNA
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<220>
<223> Primer T-T5

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taacctataa aaataggcgt atcacgaggc cc   32

<210> 49
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<212> DNA
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<220>
<223> Primer B-idi

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tcatgctgac ctggtgaagg aatcc   25

<210> 50
<211> 25
<212> DNA
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<220>
<223> Primer B-dxs(16a)

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gcgatattgt atgtctgatt cagga   25

<210> 51
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<213> Artificial sequence

<220>
<223> Primer B-lytB(16a)

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tccactggat gcgggaagct ggcag   25

<210> 52
<211> 26
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<220>
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<210> 53
<211> 25
<212> DNA
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<220>
<223> Primer B-ygb

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ccagcagcgc atgcaccgag tgttc   25

<210> 54
<211> 21
<212> DNA
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<220>
<223> Primer Tn5PCRF

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<210> 55
<211> 21
<212> DNA
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cgagcaagac gtttcccgtt g   21

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<220>
<223>   Primer Kan-2 FP-1

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acctacaaca aagctctcat caacc   25

<210>   57
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<220>
<223>   Primer Kan-2 RP-1

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